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Animal Industry Report

Animal Industry Report

AS 664

ASL R3222

2018

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Recommended Citation

Saatchi, Mahdi (2018) "Discovery of Functional Variants Remarkably Associated with Growth Traits in Several US Beef Cattle Populations," *Animal Industry Report*: AS 664, ASL R3222.
DOI: https://doi.org/10.31274/ans_air-180814-469
Available at: https://lib.dr.iastate.edu/ans_air/vol664/iss1/20

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Discovery of Functional Variants Remarkably Associated with Growth Traits in Several US Beef Cattle Populations

A.S. Leaflet R3222

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Summary and Implications

The objective of this study was to investigate the impact of some 96 putative functional variants on growth traits in beef cattle. Some 5,964 Simmental, 2,982 Gelbvieh and 2,871 Red Angus animals were genotyped and recorded for birth, weaning and yearling weights. Some functional variants in the HMGA2, NCAPG, ARRDC3, PLAG1 and ERGIC1 genes were among the markers significantly associated with remarkable impact on body weights. The most significant variant was rs109570900 encoding p.Ile442Met in NCAPG, where animals with GG compare to TT genotypes were on average 4.4 lb heavier at birth, 16.7 lb heavier at weaning and 35.7 lb heavier at yearling. Knowledge of such functional variants would create new opportunities for the selection of animals with appropriate body weights for harvest or maternal purposes and could decrease dystocia in beef cattle population.

Introduction

The DNA assays can be used to genotype cattle for more than 50,000 single nucleotide polymorphisms (SNPs) across the genome. The resulting SNP markers can be used to produce genomic enhanced estimated breeding values (GE-EBV) for selection candidates that do not necessarily have phenotypes. Even though the efficacy of within-breed genomic predictions using high-density SNP arrays such as the Illumina BovineSNP50 looks promising, their applications for across-breed genomic predictions are limited. For the technology to be fully utilized in the beef industry, across-breed and multi-breed genomic predictions must also be developed. The discovery and incorporation of functional variants with the consistent effects across different breeds could improve the across-breed and multi-breed genomic predictions in beef cattle.

In beef cattle, body weight is an important trait and optimizing size at various ages is of key economic interest. In our previous study, we identified some large-effect pleiotropic QTLs located on chromosomes BTA5, 6, 7, 14, 20 and 24 associated with body weights in several beef breeds. Some 96 putative functional variants of candidate genes in the QTL regions were selected from the dbSNP to investigate their potential impact on pre- and post-natal growth in beef cattle.

Materials and Methods

The 96 putative functional variants assayed into the new versions of GeneSeek Genomic Profilers (GGP-LD, GGP-UHD and GGP-50K). Some 5,964 Simmental, 2,982 Gelbvieh and 2,871 Red Angus animals were genotyped with one of these assays and recorded for birth, weaning and yearling weights. An association study was performed using linear mixed model in GEMMA software. The numerator relationship matrix based on the pedigree information was used to account for familiar and population structure.

Results and Discussions

Some functional variants including rs385670251 encoding p.Ala64Pro in HMGA2, rs109570900 encoding p.Ile442Met in NCAPG, rs109901274 encoding p.Tyr182Cys in ARRDC3, rs136369910 encoding g.25019900A>G in PLAG1 and rs43350563 encoding c.322G>A in ERGIC1 were among the significantly associated markers with remarkable consistent impact on body weights in all three populations (Tables 1-5).

The phenotypic variance explained by these 96 markers (chip heritability) was significant and remarkable for most growth traits in these populations (Table 6).

These new functional variants will be included into the future genetic evaluations of the International Genetic Solutions (IGS), which is a home for international genetic evaluations of 12 breed associations across the world.

Table 1 – The allele substitution effects of allele "G" of the functional variant rs109570900 encoding p.Ile442Met in NCAPG gene on growth traits in several US beef populations.

Population	Birth Weight (lb)	Weaning Weight (lb)	Yearling Weight (lb)
Simmental	2.1±.2	10.0±1.1	18.6±2.0
Red Angus	2.4±.3	6.9±1.6	19.1±3.1
Gelbvieh	2.1±.2	8.1±1.4	15.9±2.4

Table 2 – The allele substitution effects of allele "T" of the functional variant rs109901274 encoding p.Tyr182Cys in ARRDC3 on growth traits in several US beef populations.

Population	Birth Weight (lb)	Weaning Weight (lb)	Yearling Weight (lb)
Simmental	1.0±.2	3.3±1.2	9.3±2.0
Red Angus	1.3±.3	8.2±1.7	11.5±3.5
Gelbvieh	0.6±.2	3.5±1.5	9.8±2.4

Table 3 – The allele substitution effects of allele "G" of the functional variant rs43350563 encoding c.322G>A in ERGIC1 on growth traits in several US beef populations.

Population	Birth Weight (lb)	Weaning Weight (lb)	Yearling Weight (lb)
Simmental	1.5±.2	5.0±1.3	13.2±2.2
Red Angus	1.5±.3	4.6±1.6	16.3±3.0
Gelbvieh	.5±.2	3.1±1.4	9.7±2.4

Table 4 – The allele substitution effects of allele "A" of the functional variant rs136369910 encoding g.25019900A>G in PLAG1 on growth traits in several US beef populations.

Population	Birth Weight (lb)	Weaning Weight (lb)	Yearling Weight (lb)
Simmental	0.8±.2	5.4±1.3	9.1±2.2
Red Angus	2.9±.4	6.3±2.4	12.5±4.8
Gelbvieh	1.1±.2	2.1±1.5	10.0±2.6

Table 5 – The allele substitution effects of allele "C" of the functional rs385670251 encoding p.Ala64Pro in HMGA2 on growth traits in several US beef populations.

Population[1]	Birth Weight (lb)	Weaning Weight (lb)	Yearling Weight (lb)
Simmental	4.0±.8	13.0±5.5	18.8±9.1
Red Angus	-	-	-
Gelbvieh	-	-	-

[1]This variant is not segregating in the Red Angus and Gelbvieh populations.

Table 6 – The phenotypic variance explained by 96 functional variants within the candidate genes (Chip Heritability) for growth traits in several US beef populations.

Population	Birth Weight	Weaning Weight	Yearling Weight
Simmental	.15±.02	.05±.02	.10±.02
Red Angus	.11±.03	.09±.03	.00±.03
Gelbvieh	.07±.03	.01±.02	.03±.03